IN THE CLAIMS

1. (currently amended) A method of detecting cancer cells in a biological sample from a mammal, the method comprising steps of:

(i) providing the biological sample from the mammal; and

(ii) detecting a nucleic acid molecule that encodes a PRC17 polypeptide~~, comprising at least 95% amino acid sequence identity to~~ which comprises the amino acid sequence of SEQ ID NO:2 or a polymorphic variant thereof in the biological sample, wherein an increase in the level of the nucleic acid molecule in the sample compared to normal indicates the presence of cancer cells.

2. (previously presented) The method of claim 1, wherein the polypeptide has the amino acid sequence of SEQ ID NO:2.

3. (original) The method of claim 1, wherein the detecting step further comprises:

(a) contacting the nucleic acid molecule with a probe under conditions in which the probe selectively hybridizes to the nucleic acid molecule to form a stable hybridization complex; and

(b) detecting the hybridization complex.

4. (previously presented) The method of claim 3, wherein the contacting step further comprises a step of amplifying the nucleic acid in an amplification reaction.

5. (original) The method of claim 4, wherein the amplification reaction is a polymerase chain reaction.

6. (original) The method of claim 1, wherein the nucleic acid is an mRNA.

7. (original) The method of claim 1, wherein the biological sample is a tissue biopsy.

8. (original) The method of claim 7, wherein the cancer cells are selected from the group consisting of prostate tissue, breast tissue, lung tissue, and ovarian tissue.

9. (original) The method of claim 1, wherein the mammal is a human.

10. (withdrawn) A method of detecting a presence of cancer cells in a biological sample from a mammal, the method comprising steps of:

(i) providing the biological sample from the mammal; and

(ii) detecting an overexpression of a polypeptide comprising polypeptide comprising at least 85% amino acid sequence identity to an amino acid sequence of SEQ ID NO:2 or at least 70% amino acid identity to an amino acid sequence of SEQ ID NO:4 or SEQ ID NO:6 in the biological sample, thereby detecting the presence of cancer cells in the biological sample.

11. (withdrawn) The method of claim 10, wherein the polypeptide has an amino acid sequence of SEQ ID NO:2, SEQ ID NO:4 or SEQ ID NO:6.

12. (withdrawn) The method of claim 10, wherein the polypeptide is detected using an antibody that selectively binds to the polypeptide.

13. (withdrawn) The method of claim 10, wherein the biological sample is a tissue biopsy.

14. (withdrawn) The method of claim 10, wherein the cancer cells are selected from the group consisting of prostate cancer cells, breast cancer cells, lung cancer cells, and ovarian cancer cells.

15. (withdrawn) The method of claim 10, wherein the mammal is a human.

16. (withdrawn) A method of monitoring the efficacy of a therapeutic treatment of a cancer, the method comprising the steps of:

(i) providing a biological sample from a mammal undergoing the therapeutic treatment; and

(ii) detecting a level of a polypeptide comprising at least 85% amino acid sequence identity to an amino acid sequence of SEQ ID NO:2 or at least 70% amino acid identity to an amino acid sequence of SEQ ID NO:4 or SEQ ID NO:6 in the biological sample compared to a level in a biological sample from the mammal prior to, or earlier in, the therapeutic treatment, thereby monitoring the efficacy of the therapy.

17. (withdrawn) The method of claim 16, wherein the polypeptide has an amino acid sequence of SEQ ID NO:2, SEQ ID NO:4 or SEQ ID NO:6.

18. (withdrawn) The method of claim 16, wherein the cancer is selected from the group consisting of prostate cancer, ovarian cancer, lung cancer, and breast cancer.

19. (withdrawn) The method of claim 16, wherein the polypeptide is detected using an antibody that selectively binds to the polypeptide.

20. (withdrawn) A method of monitoring the efficacy of a therapeutic treatment of a cancer, the method comprising the steps of:

(i) providing a biological sample from a mammal undergoing the therapeutic treatment; and

(ii) detecting a nucleic acid molecule encoding a PRC17 polypeptide comprising at least 85% amino acid sequence identity to an amino acid sequence of SEQ ID NO:2 or at least 70% amino acid identity to an amino acid sequence of SEQ ID NO:4 or SEQ ID

NO:6 in the biological sample compared to a level in a biological sample from the mammal prior to, or earlier in, the therapeutic treatment, thereby monitoring the efficacy of the therapy.

21-43. (canceled)

44. (previously presented) The method of claim 1, wherein the nucleic acid comprises the nucleic acid sequence set forth in SEQ ID NO:1.